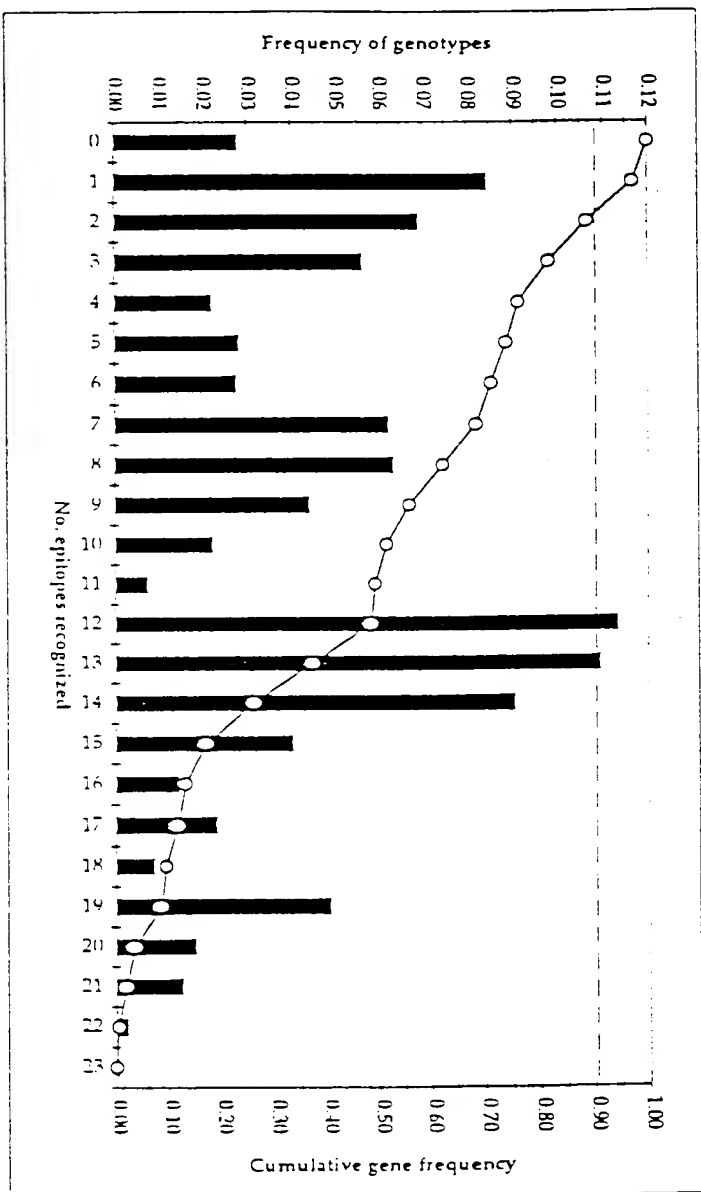


Figure 1. Monte Carlo population coverage analysis for HCV candidate epitopes



Plot of total frequency of genotypes as a function of the number of HCV candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population. One peptide, 24 0086, was not incorporated into the present analysis.

Figure 2

# HCV Minigene

## CTL Epitopes

1																	
Core 43		NS4 1590		NS3 1128		NS5 2611		Core 169		NS1/E2 632		NS4 1765		NS4 1863		Core 132	
Kozak	SigSeq	1073.11	1013.02	1069.62	1090.22	1145.12	1073.13	24.0092	1073.10	1013.10							
A3	A2	A1			A2		B7		A3		A24		A3		A2		

NS3 1258	NS4 1921	1437	NS5 2641	1466
1283.21	1283.44	35.0106	1283.55	35.0107
DR	DR	DR3	DR	DR3

## HTL Epitopes